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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2011; month=1; day=19; hr=11; min=15; sec=41; ms=273;]

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Application No: 10561040

Version No: 2.0

Input Set:

Output Set:

Started: 2011-01-13 17:01:28.567

Finished: 2011-01-13 17:01:31.636

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 69 ms

Total Warnings: 23

Total Errors: 0

No. of SeqIDs Defined: 23

Actual SeqID Count: 23

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2011-01-13 17:01:28.567
Finished: 2011-01-13 17:01:31.636
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 69 ms
Total Warnings: 23
Total Errors: 0
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)
W 402	Undefined organism found in <213> in SEQ ID (23)

SEQUENCE LISTING

<110> MIYAWAKI, ATSUSHI
 TSUTSUI, HIDEKAZU
 KARASAWA, SATOSHI

<120> FLUORESCENT PROTEIN

<130> P28994

<140> 10561040

<141> 2006-10-16

<150> PCT/JP04/08790

<151> 2004-06-16

<150> JP 2003-170330

<151> 2003-06-16

<160> 23

<170> PatentIn version 3.5

<210> 1

<211> 227

<212> PRT

<213> Favia favaus

<400> 1

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		20						25					30		

Pro	Phe	Glu	Gly	Ile	Gln	Asn	Met	Asp	Leu	Thr	Val	Ile	Glu	Gly	Gly
		35					40					45			

Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Thr	Thr	Val	Phe	Asp	Tyr	Gly
	50					55					60				

Asn	Arg	Val	Phe	Val	Lys	Tyr	Pro	Glu	Glu	Ile	Val	Asp	Tyr	Phe	Lys
65					70					75					80

Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Ser	Trp	Glu	Arg	Ser	Met	Ser	Tyr	Glu
				85					90					95	

Asp	Gly	Gly	Ile	Cys	Leu	Ala	Thr	Asn	Asn	Ile	Thr	Met	Lys	Lys	Asp
								100				105			110

Gly Ser Asn Cys Phe Val Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe
115 120 125

Pro Ala Asn Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
130 135 140

Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160

Asn Met Ala Leu Leu Leu Gln Gly Gly Gly His Tyr Arg Cys Asp Phe
165 170 175

Arg Thr Thr Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His
180 185 190

Phe Val Asp His Arg Ile Glu Ile Thr Ser His Asp Lys Asp Tyr Asn
195 200 205

Lys Val Lys Leu Tyr Glu His Ala Lys Ala His Ser Gly Leu Pro Arg
210 215 220

Leu Ala Lys
225

<210> 2
<211> 684
<212> DNA
<213> Favia favus

<220>
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Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
20 25 30

cct ttc gag gga ata cag aat atg gac ctg aca gtc ata gag ggc gga 144
Pro Phe Glu Gly Ile Gln Asn Met Asp Leu Thr Val Ile Glu Gly Gly
35 40 45

cct ctt cct ttt gct ttc gat atc ctg aca aca gta ttc gat tac ggc 192

Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Thr	Thr	Val	Phe	Asp	Tyr	Gly		
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aac	cgg	gta	ttt	gtc	aaa	tac	cca	gaa	gaa	ata	gta	gac	tac	ttc	aag		240
Asn	Arg	Val	Phe	Val	Lys	Tyr	Pro	Glu	Glu	Ile	Val	Asp	Tyr	Phe	Lys		
65					70					75					80		
cag	tcg	ttt	cct	gag	ggg	tat	tct	tgg	gaa	cga	agc	atg	agt	tac	gaa		288
Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Ser	Trp	Glu	Arg	Ser	Met	Ser	Tyr	Glu		
				85					90					95			
gac	ggg	gga	att	tgc	ctc	gcc	aca	aac	aat	ata	acg	atg	aag	aaa	gac		336
Asp	Gly	Gly	Ile	Cys	Leu	Ala	Thr	Asn	Asn	Ile	Thr	Met	Lys	Lys	Asp		
			100					105					110				
ggc	agc	aac	tgt	ttt	gtc	tat	gaa	att	cga	ttt	gat	ggg	gtg	aac	ttt		384
Gly	Ser	Asn	Cys	Phe	Val	Tyr	Glu	Ile	Arg	Phe	Asp	Gly	Val	Asn	Phe		
		115					120				125						
cct	gcc	aat	ggg	cca	gtt	atg	cag	agg	aag	acc	gtc	aaa	tgg	gag	cca		432
Pro	Ala	Asn	Gly	Pro	Val	Met	Gln	Arg	Lys	Thr	Val	Lys	Trp	Glu	Pro		
		130				135					140						
tcc	act	gag	aaa	atg	tat	gtg	cgt	gat	gga	gtg	ctg	aag	ggg	gat	gtt		480
Ser	Thr	Glu	Lys	Met	Tyr	Val	Arg	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val		
145					150					155					160		
aac	atg	gct	ctg	ttg	ctt	caa	gga	ggg	ggc	cat	tac	cga	tgt	gac	ttc		528
Asn	Met	Ala	Leu	Leu	Leu	Gln	Gly	Gly	Gly	His	Tyr	Arg	Cys	Asp	Phe		
			165					170					175				
aga	act	act	tac	aaa	gca	aag	aag	gtt	gtc	cag	ttg	cca	gac	tat	cac		576
Arg	Thr	Thr	Tyr	Lys	Ala	Lys	Lys	Val	Val	Gln	Leu	Pro	Asp	Tyr	His		
			180					185					190				
ttc	gtg	gat	cat	cga	att	gag	ata	aca	agc	cat	gac	aag	gat	tac	aac		624
Phe	Val	Asp	His	Arg	Ile	Glu	Ile	Thr	Ser	His	Asp	Lys	Asp	Tyr	Asn		
		195				200					205						
aag	gtt	aag	ctg	tat	gag	cat	gct	aaa	gct	cat	tcc	ggg	ctg	cca	agg		672
Lys	Val	Lys	Leu	Tyr	Glu	His	Ala	Lys	Ala	His	Ser	Gly	Leu	Pro	Arg		
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ctg	gcc	aag	taa														684
Leu	Ala	Lys															
225																	

<210> 3

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<220>
<221> modified_base
<222> (3)..(3)
<223> Inosine

<220>
<221> modified_base
<222> (9)..(9)
<223> Inosine

<220>
<221> modified_base
<222> (21)..(21)
<223> a, c, t, g, unknown or other

<400> 3
ggnwsbgtna ayggvcayda ntt

23

<210> 4
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 4
aactggaaga attcgcggcc gcaggaa

27

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (11)..(11)
<223> Inosine

<220>
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<222> (14)..(14)
<223> Inosine

<220>
<221> modified_base
<222> (20)..(20)
<223> Inosine

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tgccwttttgc nttngayatn ttg

23

<210> 6
<211> 35
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (4)..(4)
<223> Inosine

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<222> (15)..(15)
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<220>
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<222> (18)..(18)
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<220>
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<222> (21)..(21)
<223> Inosine

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35

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

<220>
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<223> Inosine

 <220>
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 <223> Inosine

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 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
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 <400> 8
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 <210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
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 <400> 9
 ggccacgcgt cgactagtac 20

 <210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

primer

<400> 11

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44

<210> 12

<211> 227

<212> PRT

<213> *Favia fava*

<400> 12

Met Ser Val Ile Thr Ser Glu Met Lys Met Glu Leu Arg Met Glu Gly
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Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
20 25 30

Pro Phe Glu Gly Ile Gln Asn Met Asp Leu Thr Val Ile Glu Gly Gly
35 40 45

Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Val Phe His Tyr Gly
50 55 60

Asn Arg Val Phe Val Lys Tyr Pro Glu Glu Ile Val Asp Tyr Phe Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr Glu
85 90 95

Asp Gly Gly Ile Cys Leu Ala Thr Asn Asn Ile Thr Met Lys Lys Asp
100 105 110

Gly Ser Asn Cys Phe Val Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe
115 120 125

Pro Ala Asn Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
130 135 140

Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160

Asn Met Ala Leu Leu Leu Gln Gly Gly Gly His Tyr Arg Cys Asp Phe
165 170 175

Arg Thr Thr Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His

180

185

190

Phe Val Asp His Arg Ile Glu Ile Thr Ser His Asp Lys Asp Tyr Asn
 195 200 205

Lys Val Lys Leu Tyr Glu His Ala Lys Ala His Ser Gly Leu Pro Arg
 210 215 220

Leu Ala Lys
 225

<210> 13

<211> 684

<212> DNA

<213> *Favia fava*

<220>

<221> CDS

<222> (1)..(681)

<400> 13

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 Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
 20 25 30

cct ttc gag gga ata cag aat atg gac ctg aca gtc ata gag ggc gga 144
 Pro Phe Glu Gly Ile Gln Asn Met Asp Leu Thr Val Ile Glu Gly Gly
 35 40 45

cct ctt cct ttt gct ttc gat atc ctg aca aca gta ttc cat tac ggc 192
 Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Val Phe His Tyr Gly
 50 55 60

aac cgg gta ttt gtc aaa tac cca gaa gaa ata gta gac tac ttc aag 240
 Asn Arg Val Phe Val Lys Tyr Pro Glu Glu Ile Val Asp Tyr Phe Lys
 65 70 75 80

cag tcg ttt cct gag ggt tat tct tgg gaa cga agc atg agt tac gaa 288
 Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr Glu
 85 90 95

gac ggg gga att tgc ctc gcc aca aac aat ata acg atg aag aaa gac 336
 Asp Gly Gly Ile Cys Leu Ala Thr Asn Asn Ile Thr Met Lys Lys Asp
 100 105 110

ggc agc aac tgt ttt gtc tat gaa att cga ttt gat ggt gtg aac ttt 384
 Gly Ser Asn Cys Phe Val Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe
 115 120 125

cct gcc aat ggt cca gtt atg cag agg aag acc gtc aaa tgg gag cca	432
Pro Ala Asn Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro	
130 135 140	

tcc act gag aaa atg tat gtg cgt gat gga gtg ctg aag ggt gat gtt	480
Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	

aac atg gct ctg ttg ctt caa gga ggt ggc cat tac cga tgt gac ttc	528
Asn Met Ala Leu Leu Leu Gln Gly Gly Gly His Tyr Arg Cys Asp Phe	
165 170 175	

aga act act tac aaa gca aag aag gtt gtc cag ttg cca gac tat cac	576
Arg Thr Thr Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His	
180 185 190	

ttc gtg gat cat cga att gag ata aca agc cat gac aag gat tac aac	624
Phe Val Asp His Arg Ile Glu Ile Thr Ser His Asp Lys Asp Tyr Asn	
195 200 205	

aag gtt aag ctg tat gag cat gct aaa gct cat tcc ggg ctg cca agg	672
Lys Val Lys Leu Tyr Glu His Ala Lys Ala His Ser Gly Leu Pro Arg	
210 215 220	

ctg gcc aag taa	684
Leu Ala Lys	
225	

<210> 14
 <211> 227
 <212> PRT
 <213> Favia favus

<400> 14
Met Ser Val Ile Thr Ser Glu Met Lys Met Glu Leu Arg Met Glu Gly
1 5 10 15

Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
20 25 30

Pro Phe Glu Gly Ile Gln Asn Val Asp Leu Thr Val Ile Glu Gly Gly
35 40 45

Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Val Phe His Tyr Gly
50 55 60

Asn Arg Val Phe Val Lys Tyr Pro Glu Glu Ile Val Asp Tyr Phe Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr Glu

85

90

95

Asp Gly Gly Ile Cys Leu Ala Thr Asn Asn Ile Thr Met Lys Lys Asp
 100 105 110

Gly Ser Asn Cys Phe Val Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe
 115 120 125

Pro Ala Asn Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
 130 135 140

Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

Asn Met Ala Leu Leu Leu Gln Gly Gly Gly His Tyr Arg Cys Asp Phe
 165 170 175

Arg Thr Thr Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His
 180 185 190

Phe Val Asp His Arg Met Glu Ile Thr Ser His Asp Lys Asp Tyr Asn
 195 200 205

Lys Val Lys Leu Tyr Glu His Ala Lys Ala His Ser Gly Leu Pro Arg
 210 215 220

Leu Ala Lys
 225

<210> 15

<211> 684

<212> DNA

<213> Favia favus

<220>

<221> CDS

<222> (1)..(681)

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gct gta aac ggg cac aag ttc gtg att aca ggg aaa gga agt ggc cag 96
 Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly Gln
 20 25 30

cct ttc gag gga ata cag aat gtg gac ctg aca gtc ata gag ggc gga	144
Pro Phe Glu Gly Ile Gln Asn Val Asp Leu Thr Val Ile Glu Gly Gly	
35 40 45	
cct ctt cct ttt gct ttc gat atc ctg aca aca gta ttc cat tac ggc	192
Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Val Phe His Tyr Gly	
50 55 60	
aac cgg gta ttt gtc aaa tac cca gaa gaa ata gta gac tac ttc aag	240
Asn Arg Val Phe Val Lys Tyr Pro Glu Glu Ile Val Asp Tyr Phe Lys	
65 70 75 80	
cag tcg ttt cct gag ggt tat tct tgg gaa cga agc atg agt tac gaa	288
Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr Glu	
85 90	